Amendments to the Specification:

Page 4, under line 10, insert:

Summary of the Invention

Page 33, under line 2, insert:

Brief Description of the Drawings

Page 35, lines 7-14, replace the entire paragraph with the following amended paragraph:

The complete organization of the *asap* gene and its chromosomal localization were obtained by comparing the sequence of the cDNA obtained in example 1, with the sequence of the human genome, using the Wellcome Trust Sanger Institute programs ~~(http://www.ensembl.oriz/genome/central/~~ and more particularly the BLAST search program ~~(http://genome.cse.ucsc.edu/)~~.

Page 35, lines 16-27, replace the entire paragraph with the following amended paragraph:

The human *asap* gene consists of 29750 nucleotides comprising 14 exons, only 13 of which are translated, the first exon not being translated. The size of the exons ranges from 71 to 321 base pairs. The sequence of the gene is contained in the contig AC097467 (length 178204 base pairs) between bases 115117 and 143828 (version v.7.29a3 NCBI/Ensembl of July 12, 2002, ~~http://www.ensembl.org)~~ and is, moreover, located on chromosome 4q32.1 between the anonymous markers D4S1053 and D4S571 (region 161.25 megabases (Mb) to 161.28 Mb). The sequence of the gene is physically contained in the BAC clone RP11-27G13.

Page 36, lines 8-24 and page 37, lines 1-3, replace the entire paragraph continuing on page 37 with the following amended paragraph:

The protein sequence was compared to the databank sequences using the PSI-BLAST programs of the NCBI ~~(http://www.ncbi.nlm.nh.gov/Sitemap/)~~. Consensus protein motifs were sought using the DART programs of the NCBI and the SMART program of ExPASy-Tools ~~(http://www.expasy.ch/tools/#similariw)~~, the parameters of which make is possible to detect

motifs with weak homology. The ASAP protein exhibits a sequence identity of 23% over the C-terminal third with a microtubule-associated protein (MAP 1A, for microtubule-associated protein 1A). Moreover, the search for conserved motifs (DART or SMART) reveals domains of caldesmon type (N.B. Gusev, Biochemistry, 10 1112-1121, 2000) and ERM type (ezrin/radixin/moesin) (Louvet-Vallet, S., Biol. Cells. 274: 305-316, 2000), which are proteins that are also considered to be MAPs, with identities of approximately 20%. It also has a BRCT domain (breast cancer carboxy-terminal domains; P. Bork et al., J. FASEB, 11, 6876 (1997)) between positions 65 and 303.

Page 37, lines 11-17, replace the entire paragraph with the following amended paragraph:

Computer analysis of the protein using the programs accessible on the Internet site ~~(http://npsa-bil.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_se-cons.html)~~ reveals that it lacks β-sheets and is very rich in α-helices, in particular in the region between amino acids 420-620, which is almost exclusively made up of α-helices.